



# NCBI Conserved Domain Summary

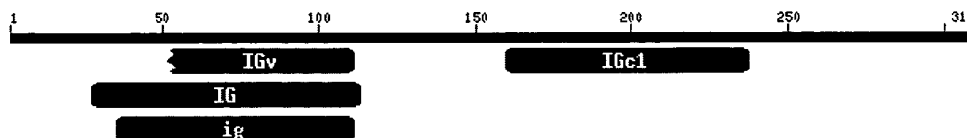
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RPS-BLAST 2.2.4 [Aug-26-2002]

Query= [gi|339012|gb|AAA61027.1|](#) T-cell receptor precursor  
(310 letters)

Database: oasis\_sap.v1.58  
4540 PSSMs; 885,521 total columns

Click on boxes for multiple alignments



Domain Relatives

- .. This CD alignment includes 3D structure. To display structure, download [Cn3D!](#)

PSSMs producing significant alignments:

Score E  
(bits) value

<a href="#">gnl CDD 3898</a>	smart00407, IGc1, Immunoglobulin C-Type;	<a href="#">75.3</a>	3e-15
<a href="#">gnl CDD 3897</a>	smart00406, IGv, Immunoglobulin V-Type;	<a href="#">41.5</a>	4e-05
<a href="#">gnl CDD 7359</a>	smart00409, IG, Immunoglobulin;	<a href="#">40.1</a>	9e-05
<a href="#">gnl CDD 7427</a>	pfam00047, ig, Immunoglobulin domain. Members of the immunoglo...	<a href="#">40.3</a>	9e-05

- [gnl|CDD|3898](#), smart00407, IGc1, Immunoglobulin C-Type;

CD-Length = 75 residues, 98.7% aligned  
Score = 75.3 bits (185), Expect = 3e-15

```
Query: 159 KATLVCLATGIFPDHVELSWVNGKEVHSGVSTDPQPLKEQPALNDSRYCLSSRLRVSAT 218
Sbjct: 1 PATLVCLVTGFYPDPDITVTWLKNGQEVTSVSTTDPLKDK-----DGTYFLSSYLTVSAS 55

Query: 219 FWQNPРНHFRСQVQFYGLSE 238
Sbjct: 56 TW-ESGDVYTCQVTHEGLTE 74
```

- [gnl|CDD|3897](#), smart00406, IGv, Immunoglobulin V-Type;

CD-Length = 80 residues, only 77.5% aligned  
Score = 41.5 bits (97), Expect = 4e-05

```
Query: 51 LYWYRQTLGQGPEFLTYFQNEAQLEKSRLLSDRFSAER--PKGSFSTLEIQRTQGDСAM 108
Sbjct: 18 VSWVRQPPGKGLEWLGYIGSDVSYSEA-SYKGRVTISKDNSKNDV-SLTISNLRVEDTGT 75

Query: 109 YLCA 112
Sbjct: 76 YYCA 79
```

- [gnl|CDD|7359](#), smart00409, IG, Immunoglobulin;

CD-Length = 86 residues, 82.6% aligned  
Score = 40.1 bits (93), Expect = 9e-05

Query: 27 PRHNITKRGQNVTFRCDPIS-EHNRLYWYRQTLGQGPEFLTYFQNEAQLEKSRLLSDRFS 85  
Sbjct: 1 PPSVTVKEGESVTLSCASGNPPPEVTWYKQ--GSKLAY-----SGRFS 43

Query: 86 AERPKGFSFSTLEIQRTEQGDSAMYLCASS 114  
Sbjct: 44 VSRSGGNS-TLTISNVTPEDSGTYTCAAT 71

gnl|CDD|7427, pfam00047, ig, Immunoglobulin domain. Members of the immunoglobulin superfamily are found in hundreds of proteins of different functions. Examples include antibodies, the giant muscle kinase titin and receptor tyrosine kinases. Immunoglobulin-like domains may be involved in protein-protein and protein-ligand interactions. The Pfam alignments do not include the first and last strand of the immunoglobulin-like domain.

CD-Length = 66 residues; 98.5% aligned  
Score = 40.3 bits (93), Expect = 9e-05

Query: 35 GQNVTFRC--DPIS EHNRLYWYRQTLGQGPEFLTYFQNEAQLEKSRLLSDRFSAERP KGS 92  
Sbjct: 1 GESVTLTCSVSGYPPDPTVTWLRNGKELELGVLVTS-----SSSGRTSTS 45

Query: 93 FSTLEIQRTEQGDSAMYLCA 112  
Sbjct: 46 SLSLTISSVTPEDSGTYTCV 65

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